

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2003, 16:11:58 ; Search time 9.77143 Seconds
(without alignments)
91.441 Million cell updates/sec

Title: US-09-905-691-2
Perfect score: 19
Sequence: 1 ARAARRARARARARAE 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 127863 seqs, 47026705 residues
Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	1	7	36.8	145	1 YV40_DEIRA	Q9Z84 deinococcus
2	2	7	36.8	193	1 VCO7_ADE04	Q96831 human adeno
3	3	7	36.8	263	1 CMC_BRAJA	P30962 bradyrhizob
4	4	7	36.8	291	1 YN32_MYCTU	Q10515 mycobacteri
5	5	7	36.8	326	1 Y083_CAUCR	P37895 caulobacter
6	6	7	36.8	362	1 CKRA_HUMAN	P46092 homo sapien
7	7	7	36.8	381	1 ARGJ_THETH	P96137 thermus the
8	8	7	36.8	383	1 SUC2_STRCO	Q87840 streptomyce
9	9	7	36.8	387	1 ARGJ_METKA	Q8TX15 m arginine
10	10	7	36.8	394	1 FXD3_CHICK	P79772 gallus gall
11	11	7	36.8	417	1 PROA_MEIRU	Q86053 meiothermus
12	12	7	36.8	423	1 CES5_HUMAN	Q9BXW7 homo sapien
13	13	7	36.8	428	1 Y486_MYCLE	P84138 mycobacteri
14	14	7	36.8	444	1 VGLX_HSVBS	Q88103 bovine herp
15	15	7	36.8	448	1 TRME_XANAC	Q9PEH9 xanthomonas
16	16	7	36.8	474	1 CYAE_BORPE	P11092 bordetella
17	17	7	36.8	480	1 Y486_MYCTU	Q11152 mycobacteri
18	18	7	36.8	499	1 GSHR_PLAF7	Q15770 plasmodium
19	19	7	36.8	499	1 GSHR_PLAFK	Q94655 plasmodium
20	20	7	36.8	521	1 EX7L_RHIL0	Q987V3 rhizobium l
21	21	7	36.8	503	1 U526_HCMVA	P09699 human cytom
22	22	7	36.8	621	1 HEM1_AGABI	Q92403 agaricus bi
23	23	7	36.8	742	1 UL47_HSVBP	P30021 bovine herp
24	24	7	36.8	777	1 METE_CAUCR	Q9AAW1 caulobacter
25	25	7	36.8	799	1 SYFE_CAUCR	Q9A9E5 caulobacter
26	26	7	36.8	913	1 VGLB_PRVIF	P08355 pseudorabie
27	27	7	36.8	1318	1 VP14_EBV	P03179 Epstein-bar
28	28	7	36.8	1394	1 HAP_HAEIN	P45387 haemophilus
29	29	7	36.8	2390	1 SPCP_HUMAN	O15020 homo sapien
30	30	7	36.8	4523	1 DYHB_HUMAN	Q96dts homo sapien
31	31	6	31.6	68	1 RPOZ_NEIMA	Q9JQ89 neisseria m
32	32	6	31.6	74	1 Y082_BPFP2	Q06424 bacterioph
33	33	6	31.6	88	1 RPOZ_HAEIN	P43740 haemophilus

34	6	31.6	89	1 RPOZ_PASMU	Q9cmb2 pasteurella
35	6	31.6	90	1 RPOZ_VIBCH	Q9kmb3 vibrio chol
36	6	31.6	90	1 RPOZ_VIBPA	Q87tb0 vibrio para
37	6	31.6	90	1 RPOZ_VIBVU	Q8ddv5 vibrio vuln
38	6	31.6	91	1 RPOZ_ECOLI	P08374 escherichia
39	6	31.6	91	1 RPOZ_YERPE	Q8zjq3 yersinia pe
40	6	31.6	94	1 R28A_MYCTU	Q10879 mycobacteri
41	6	31.6	108	1 NIFW_RHOSH	Q01182 rhodobacter
42	6	31.6	113	1 UL67_HCMVA	P16747 human cytom
43	6	31.6	117	1 RL18_HAEIN	P43556 haemophilus
44	6	31.6	117	1 VGLJ_HSVBS	P36344 simian herp
45	6	31.6	120	1 PAND_ALCEU	Q9zhi5 alcaligenes

ALIGNMENTS

RESULT 1
ID YV40_DEIRA STANDARD; PRT; 145 AA.
AC Q9Z84;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein DRB0040.
GN DRB0040.
OS Deinococcus radiodurans.
OC Plasmid MPl.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.N.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
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CC -----
CC EMBL; AE001826; AAF12646.1;
DR PIR: E75622; E75622.
DR TIGR: DRB0040;
DR InterPro; IPR001844; Chaprin_Cpn60.
RW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 145 AA; 15152 MW; B8ED52495897EC3 CRC64;

Query Match 36.8%; Score 7; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 AARRAR 9
Db 132 AARRAR 138
|||||

RESULT 2
ID VCO7_ADE04 STANDARD; PRT; 193 AA.

Q96831;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major core protein precursor (Protein VII) (pVII).
PVI.
Human adenovirus type 4.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=28280;
[1]
SEQUENCE FROM N.A.
RC STRAIN=Isolate RI-6;
RA Tarasishin L., Szawlowski P.W.S., McRay J., Russell W.C.;
RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
CC
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CC
CC EMBL: U70921; AAC83411.1;
CC InterPro: IPR004912; Adeno_VII.
CC Pfam: PF03228; Adeno_VII; 1.
CC PROPEP 1 24
CC CHAIN 25 193
CC SITE 24 25
CC
CC BY SIMILARITY.
CC MAJOR CORE PROTEIN.
CC CLEAVAGE (BY ADENOVIRUS PROTEASE)
CC (POTENTIAL).
CC
CC SEQUENCE 193 AA; 21358 MW; 43137E07DB379DD0 CRC64;
Query Match 36.8%; Score 7; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RAARRAA 8
Db 135 RAARRAA 141

RESULT 3
CCMC_BRAJA STANDARD; PRT; 263 AA.
ID CCMC_BRAJA
AC P30962;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Heme exporter protein C (Cytochrome c-type biogenesis protein cyc2).
GN CYC2 OR CCMC OR BLR0469.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobiaceae.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=110RIF15;
RC MEDLINE=91210304; PubMed=1850420;
RA Ramsesier T.M., Winteler H.V., Hennecke H.;
RT "Discovery and sequence analysis of bacterial genes involved in the
RT biogenesis of c-type cytochromes.";
RL J. Biol. Chem. 266:7793-7803(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=2248498; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasanoto S., Watanabe A., Igesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Teiruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).

-1- FUNCTION: REQUIRED FOR THE EXPORT OF HEME TO THE PERIPLASM FOR THE
CC BIOGENESIS OF C-TYPE CYTOCHROMES.
CC
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC
CC -1- SIMILARITY: BELONGS TO THE CCMC/CYCZ/HELC FAMILY.
CC
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CC
CC EMBL: M60874; AAA26194.1;
CC EMBL: AP005936; BAC45734.1;
CC FIC; C39741; C39741.
CC InterPro: IPR002541; CytC_asm.
CC Pfam: PF01578; CytC_asm; 1
CC PRINTS: PR01386; CCMCBI0GNSIS.
CC TIGRFS: TIGR01191; ccmC; 1.
CC
CC Cytochrome c-type biogenesis; Transport; Transmembrane;
CC Inner membrane; Complete proteome.
CC
CC TRANSMEM 19 39
CC TRANSMEM 61 81
CC TRANSMEM 92 112
CC TRANSMEM 126 146
CC TRANSMEM 157 177
CC TRANSMEM 198 218
CC
CC SEQUENCE 263 AA; 28831 MW; A02EF7576F94EC0 CRC64;
Query Match 36.8%; Score 7; DB 1; Length 263;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 RAARRAA 12
Db 151 RAARRAA 157

RESULT 4
YM32_MYCTU STANDARD; PRT; 291 AA.
ID YM32_MYCTU
AC Q10515; Q10516;
DT 01-OCT-1996 (Rel. 34, Created)
DT 18-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein RV2232/RV2233.
GN RV2232/RV2233 OR WP2292 OR WTCY427.13/WTCY427.14.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RC MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., Mclean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Otterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CBHY/CBBZ/GPH/YIEH FAMILY.
 CC -----
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 CC -----
 DR EMBL; Z70692; CAA94656.1; ALT TERM.
 DR EMBL; Z70692; CAA94655.1; ALT_INIT.
 DR EMBL; AE007074; AAR46576.1; -
 DR TIGR; MT2292; -
 DR TuberculList; RV2232; -
 DR TuberculList; RV2233; -
 DR InterPro; IPR005834; Hydrolase.
 DR Pfam; PF00702; Hydrolase; 1.
 DR KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 291 AA; 30694 MW; 750F090FB154E6E5 CRC64;
 Query Match 36.88; Score: 7; DB 1; Length 291;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 RAAARRA 15
 DB 66 RAAARRA 72
 RESULT 5
 Y083_CAUCR STANDARD; PRT; 336 AA.
 ID Y083_CAUCR STANDARD; PRT; 336 AA.
 AC P37895;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2003 (Rel. 42, Last annotation update)
 DE Hypothetical protein CC2483.
 GN CC2483.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
 OC Caulobacteraceae; Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=8421698;
 RA Wang S.P., Sharma P.L., Schoenlein P.V., Ely B.;
 RA "A histidine protein kinase is involved in polar organelle
 RA development in *Caulobacter crescentus*.";
 RA Proc. Natl. Acad. Sci. U.S.A. 90:630-634(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smith J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Otterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RA "Complete genome sequence of *Caulobacter crescentus*.";
 RA Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 CC -1- SIMILARITY: BELONGS TO THE ARGK FAMILY.
 CC -----

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 CC -----
 DR EMBL; M91449; AAA23053.1; -
 DR EMBL; AE005917; AAK24454.1; -
 DR PIR; B87557; B87557.
 DR PIR; S27534; S27534.
 DR TIGR; CC2483; -
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR005129; ArgK.
 DR Pfam; PF03308; ArgK; 1.
 DR SMART; SM00382; AAA; 1.
 DR TIGRFAMS; TIGR00750; laoi; 1.
 DR KW Hypothetical protein; ATP-binding; Complete proteome.
 FT NP_BIND 61 68 ATP (POTENTIAL).
 FT CONFLICT 77 77 N -> K (IN REF. 1).
 SQ SEQUENCE 326 AA; 34550 MW; 3F58765201CEF32D CRC64;
 Query Match 36.88; Score: 7; DB 1; Length 326;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARAARRA 7
 DB 264 ARAARRA 270
 RESULT 6
 CKRA_HUMAN STANDARD; PRT; 362 AA.
 ID CKRA_HUMAN STANDARD; PRT; 362 AA.
 AC P46092; Q9NZG2;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 10 (C-C CKR-10) (CC-CKR-10) (CCR-10) (G-
 DE protein coupled receptor 2).
 GN GPR2 OR CCR10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=20191997; PubMed=10725696;
 RA Jarmin D.I., Rits M., Bota D., Gerard N.P., Graham G.J.,
 RA Clark-Lewis I., Gerard C.;
 RA "Identification of the orphan receptor G-protein-coupled receptor 2 as
 RA CCR10, a specific receptor for the chemokine ESKine";
 RA J. Immunol. 164:3460-3464(2000).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=20191998; PubMed=10725697;
 RA Homey B., Wang W., Soto H., Buchanan M.E., Wiesenborn A., Catron D.,
 RA Muller A., McClanahan T.K., Dieu-Nosjean M.C., Orozco R., Ruzicka T.,
 RA Lehmann P., Oldham E., Zlotnik A.;
 RA "The orphan chemokine receptor G protein-coupled receptor-2 (GPR-2,
 RA CCR10) binds the skin-associated chemokine CCL27 (CTACK/ALP/ILC).";
 RA J. Immunol. 164:3465-3470(2000).
 RN [3]
 RP SEQUENCE OF 9-362 FROM N.A.
 RX MEDLINE=95154831; PubMed=7851889;
 RA Marchese A., Docherty J.M., Nguyen T., Heiber M., Cheng R.,
 RA Heng H.H.Q., Tsui L.-C., Shi X., George S.R., O'Dowd B.F.;
 RA "Cloning of human genes encoding novel G protein-coupled receptors";
 RA Genomics 23:609-618(1994).
 RN [4]
 RP LIGAND BINDING, AND TISSUE SPECIFICITY.
 RX MEDLINE=20357357; PubMed=10781587;

Wang W., Soto H., Oldham E.R., Buchanan M.E., Honey B., Catron D., Jenkins N., Copeland N.G., Gilbert D.J., Nguyen N., Abrams J., Karshenovich D., Smith K., McClanahan T., Vicari A.P., Zlotnik A.; *Identification of a novel chemokine (CCL28), which binds CCR10 (GPR2).*

J. Biol. Chem. 275:22313-22323(2000).

[5]

LIGAND BINDING.

MEDLINE-20432268; PubMed-10975800;

Pan J., Kunkel E.J., Gossler U., Lazarus N., Langdon P., Broadwell K., Vierra M.A., Genovese M.C., Butcher E.C., Soler D.; *A novel chemokine ligand for CCR10 and CCR3 expressed by epithelial cells in mucosal tissues*;

J. Immunol. 165:2943-2949(2000).

CC -1- FUNCTION: RECEPTOR FOR CHEMOKINES SCYA27 AND SCYA28. SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL AND STIMULATES CHEMOTAXIS IN A PRE-B CELL LINE.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN ADULT TESTIS, SMALL INTESTINE, FETAL LUNG, FETAL KIDNEY, WEAKER EXPRESSION WAS OBSERVED IN MANY OTHER ADULT TISSUES INCLUDING SPLEEN, THYMUS, LYMPH NODE, PETER'S PATCHES, COLON, HEART, OVARY, PERIPHERAL BLOOD LYMPHOCYTES, THYROID AND SPINAL CORD. ALSO EXPRESSED BY MELANOCYTES, DERMAL FIBROBLASTS, DERMAL MICROVASCULAR ENDOTHELIAL CELLS. ALSO DETECTED IN T CELLS AND IN SKIN-DERIVED LANGERHANS CELLS.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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EMBL; AF215981; AAF63709.1; -;
EMBL; AF208237; AAF72871.1; -;
EMBL; U13667; AAA64593.1; -;
Genew; HGNC:4474; GPR2.
DR MIR; 600240; -;
GO; GO:0005887; C: integral to plasma membrane; TAS.
GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; TAS.
InterPro; IPR005382; CC_chemok10.
DR IntAct; IPRO00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm.1; 1;
DR PRINTS; PR01557; CHEMOKINER10.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEPT_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 53 68 1 (POTENTIAL).
FT FT DOMAIN 69 78 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 79 99 2 (POTENTIAL).
FT FT DOMAIN 100 114 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 115 136 3 (POTENTIAL).
FT FT DOMAIN 137 159 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 160 179 4 (POTENTIAL).
FT FT DOMAIN 180 203 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 204 225 5 (POTENTIAL).
FT FT DOMAIN 226 247 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 248 269 6 (POTENTIAL).
FT FT DOMAIN 270 290 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 291 313 7 (POTENTIAL).
FT FT DOMAIN 314 362 CYTOPLASMIC (POTENTIAL).
FT FT DISULFID 113 191 BY SIMILARITY.
FT FT CONFLICT 51 51 V -> L (IN REF. 3).
FT FT CONFLICT 235 235 MISSING (IN REF. 2).
FT FT CONFLICT 330 330 S -> C (IN REF. 2).
FT FT SEQUENCE 362 AA; 38399 MW; 69DF12B639AE99A CRC64;

Query Match

```

Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AARRAAR 9
    | | | | |
Db 68 AARRAAR 74

```

RESULT 7

ARGJ_THETH ID	ARGJ_THETH STANDARD;	PRT; 381 AA.
AC	P96137;	
DT	15-SEP-2003 (Rel. 42, Created)	
DT	15-SEP-2003 (Rel. 42, Last sequence update)	
DT	15-SEP-2003 (Rel. 42, Last annotation update)	
DE	Glutamate N-acetyltransferase (EC 2.3.1.35) (Ornithine acetyltransferase) (Ornithine transacetylase) (OATase) [Contains:	
DE	Glutamate N-acetyltransferase alpha chain; Glutamate N-	
DE	acetyltransferase beta chain].	
GN	ARGJ.	
OS	Thermus thermophilus.	
OC	Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;	
OC	Thermus.	
OX	NCBI_TaxID=274;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-HB27;	
RX	MEDLINE=98154436; PubMed=9493385;	
RA	Baetens M., Legrain C., Boyen A., Glandsdorff N.;	
RA	"Genes and enzymes of the acetyl cycle of arginine biosynthesis in the	
RT	extreme thermophilic bacterium Thermus thermophilus HB27.";	
RT	Microbiology 144:479-492(1998).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-HB27;	
RA	Sanchez R., Roovers M., Glandsdorff N.;	
RT	"Organisation of arginine biosynthetic genes in Thermus	
RT	thermophilus.";	
CC	Submitted (NOV-1998) to the EMBL/GenBank/DBSJ databases.	
CC	-1- CATALYTIC ACTIVITY: N(2)-acetyl-L-ornithine + L-glutamate - L-	
CC	ornithine + N-acetyl-L-glutamate.	
CC	-1- PATHWAY: Arginine biosynthesis; fifth step.	
CC	-1- SUBUNIT: Heterotetramer of two alpha and two beta chains (By	
CC	similarity).	
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).	
CC	-1- MISCELLANEOUS: Some bacteria possess a monofunctional argJ, i.e.,	
CC	capable of catalyzing only the fifth step of the arginine	
CC	biosynthetic pathway.	
CC	-1- SIMILARITY: Belongs to the argJ family.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; Y10525; CAAY1551.1;	
DR	EMBL; Y18353; CAAY7143.1;	
DR	HAMAP; MF_01106; -;	
DR	InterPro: IPR002813; ArgJ.	
DR	Pfam: PF01960; ArgJ; 1.	
DR	ProDom; PD004193; ArgJ; 1.	
DR	TIGRFAMS; TIGR00120; ArgJ; 1.	
KW	Arginine biosynthesis; Transferrase; Acyltransferase.	
FT	CHAIN 1 175	
FT	GLUTAMATE N-ACETYLTRANSFERASE ALPHA CHAIN	
FT	(BY SIMILARITY)	
FT	GLUTAMATE N-ACETYLTRANSFERASE BETA CHAIN	
FT	(BY SIMILARITY).	
SQ	CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY). SEQUENCE 381 AA; 4A0318 MW; 1605C5B17B7B05A8 CRC64;	

Query Match 36.8%; Score 7; DB 1; Length 381;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ARAARA 10
 DB 274 ARAARA 280

RESULT 8
 SUC2_STRCO STANDARD; PRT; 383 AA.
 ID SUC2_STRCO
 AC O87840;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Succinyl-CoA synthetase beta chain 2 (EC 6.2.1.5) (SCS-beta 2).
 DE SUC2 OR SC06585 OR SC8A6.06.
 GN Streptomyces coelicolor.
 OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidaigo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).
 RL Nature 417:141-147(2002).
 CC -1- CATALYTIC ACTIVITY: ATP + succinate + CoA = ADP + succinyl-CoA +
 phosphate.
 CC -1- PATHWAY: Tricarboxylic acid cycle.
 CC -1- SUBUNIT: Composed of an alpha chain and a beta chain (By
 similarity).
 CC -1- SIMILARITY: Belongs to the succinate/malate CoA ligase beta
 subunit family.

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 EMBL; AL939128; CAA19778.1; -;
 DR F1R; T35773; T35773.
 DR HSP; P07460; 18CU.
 DR HAMAP; MF_00558; -; 1.
 DR InterPro; IPR003135; ATP-grasp.
 DR InterPro; IPR005809; CoA_lig_beta.
 DR InterPro; IPR005811; CoA_ligase.
 DR Pfam; PF02222; ATP-grasp; 1.
 DR TIGRFAMs; TIGR01016; ligase-CoA; 1.
 DR TIGRFAMs; TIGR01016; sucCoABeta; 1.
 DR PROSITE; PS01217; SUCINYL-CoA_LIG_3; 1.
 KW Ligase; Tricarboxylic acid cycle; Complete proteome.
 SQ SEQUENCE 383 AA; 40161 MW; 5A3D05C0FD1DD03 CRC64;

Query Match 36.8%; Score 7; DB 1; Length 383;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ARAARA 9

DB 365 ARAARA 371

RESULT 9
 ARGJ_METKA STANDARD; PRT; 387 AA.
 ID ARGJ_METKA
 AC Q8TX15;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Arginine biosynthesis bifunctional protein argJ [Includes: Glutamate
 N-acetyltransferase (EC 2.3.1.35) (Ornithine acetyltransferase)
 (Ornithine transacetylase) (OATase); Amino-acid acetyltransferase
 (EC 2.3.1.1) (N-acetylglutamate synthase) (AGS)] [Contains: Arginine
 biosynthesis bifunctional protein argJ alpha chain; Arginine
 biosynthesis bifunctional protein argJ beta chain].
 DE ARGJ OR MKQ865.
 GN Methanopyrus kandleri.
 OS Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
 OC Methanopyrus.
 OX NCBI_TaxID=2320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AV19 / DSM 6324 / JCM 9639;
 RX MEDLINE=21927647; PubMed=11930014;
 RA Slesarev A.I., Mezheva V.V., Makarova K.S., Polushin N.N.,
 RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
 RA Natile D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
 RA Malykh A.G., Koonin E.V., Kozavkin S.A.;
 RT The complete genome of hyperthermophile Methanopyrus kandleri AV19
 and monophyly of archaeal methanogens.
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
 CC -1- FUNCTION: Catalyzes two activities which are involved in the
 cyclic version of arginine biosynthesis: the synthesis of
 acetylglutamate from glutamate and acetyl-CoA, and of ornithine by
 transacetylation between acetylornithine and glutamate (By
 similarity).
 CC -1- CATALYTIC ACTIVITY: N(2)-acetyl-L-ornithine + L-glutamate = L-
 ornithine + N-acetyl-L-glutamate.
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + L-glutamate = CoA + N-acetyl-L-
 glutamate.
 CC -1- PATHWAY: Arginine biosynthesis; first step.
 CC -1- PATHWAY: Arginine biosynthesis; fifth step.
 CC -1- SUBUNIT: Heterotetramer of two alpha and two beta chains (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- MISCELLANEOUS: Some bacteria possess a monofunctional argJ, i.e.,
 capable of catalyzing only the fifth step of the arginine
 biosynthetic pathway.
 CC -1- SIMILARITY: Belongs to the argJ family.

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 EMBL; AE010376; AAM02078.1; -;
 DR HAMAP; MF_01106; atypical; 1.
 DR InterPro; IPR002813; ArgJ.
 DR Pfam; PF01960; ArgJ; 1.
 DR ProDom; PD004193; ArgJ; 1.
 DR TIGRFAMs; TIGR00120; ArgJ; 1.
 DR TIGRFAMs; TIGR00120; ArgJ; 1.
 KW Arginine biosynthesis; Multifunctional enzyme; Transferase;
 ACyltransferase; Complete proteome.
 CHAIN 1 172 ARGinine BIOSYNTHESIS BIFUNCTIONAL
 PROTEIN ARGJ ALPHA CHAIN (BY SIMILARITY).
 CHAIN 173 387 ARGinine BIOSYNTHESIS BIFUNCTIONAL
 PROTEIN ARGJ BETA CHAIN (BY SIMILARITY).
 SQ SEQUENCE 387 AA; 41840 MW; ED311EC1F47D56DD CRC64;

Query Match 36.8%; Score 7; DB 1; Length 387;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ARRAARA 10
 DB 276 ARRAARA 282

RESULT 10

FXD3_CHICK STANDARD; PRT; 394 AA.
 AC P79772;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Forkhead box protein D3 (HNF3/FH transcription factor, genesis) (Winged
 helix protein CWH-3).
 GN FOXD3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=97141794; PubMed=8988052;
 RA Freyaldenhoven B.S., Freyaldenhoven M.P., Iacovoni J.S., Vogt P.K.;
 RT "Aberrant cell growth induced by avian winged helix proteins.";
 RL Cancer Res. 57:123-129(1997).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: Contains 1 fork-head domain.

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EMBL: U37274; AAC60066.1; -
 DR HSSP; Q63245; 2HFH.
 DR TRANSFAC; T02495; -
 DR InterPro: IPR001765; TF_Fork_head.
 DR Pfam; PF00250; Fork_head; 1.
 DR PRINTS; PR00053; FORKHEAD.
 DR ProDom; PD000425; TF_Fork_head; 1.
 DR SMART; SM00339; FH; 1.
 DR PROSITE; PS00657; FORK_HEAD_1; 1.
 DR PROSITE; PS00658; FORK_HEAD_2; 1.
 DR PROSITE; PS50039; FORK_HEAD_3; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 FT DOMAIN 67 70 POLY-ALA.
 FT DOMAIN 80 91 POLY-GLY.
 FT DOMAIN 100 106 POLY-ALA.
 FT DNA_BIND 117 211 FORK-HEAD.
 SQ SEQUENCE 394 AA; 40995 MW; 324A4B36B9E31899 CRC64;

Query Match 36.8%; Score 7; DB 1; Length 394;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAARRAA 8
 DB 62 RAARRAA 68

RESULT 11

PROA_MEIRU

ID PROA_MEIRU STANDARD; PRT; 417 AA.
 AC O86033;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-
 semialdehyde dehydrogenase) (Glutamyl-gamma-semialdehyde
 dehydrogenase) (GSA dehydrogenase).
 GN PROA.
 OS Meiothermus ruber.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Meiothermus.
 OX NCBI_TaxID=277;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=40;
 RA Yaklichkin S.Y., Zimina M.S., Yurchenko Y.V., Hromov I.S.,
 RT "Molecular cloning and sequence analysis of the proA gene from
 thermophilic eubacterium Thermus ruber.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE NADPH DEPENDENT REDUCTION OF L-GAMMA-
 GLUTAMYL 5-PHOSPHATE INTO L-GLUTAMATE 5-SEMIALDEHYDE AND
 PHOSPHATE. THE PRODUCT SPONTANEOUSLY UNDERGOES CYCLIZATION TO-FORM
 1-PYRROLINE-5-CARBOXYLATE.
 CC -1- CATALYTIC ACTIVITY: L-glutamate 5-semialdehyde + phosphate +
 NADP(+) -> L-gamma-glutamyl 5-phosphate + NADPH.
 CC -1- PATHWAY: Proline biosynthesis; second step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE GAMMA-GLUTAMYL PHOSPHATE REDUCTASE
 FAMILY.

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EMBL: AF082661; AAC72811.1; -
 DR HAMAP; MF_00412; -; 1.
 DR InterPro: IPR002086; Aldehyde_dehydr.
 DR InterPro: IPR000965; Gglut_pp_reduct.
 DR Pfam; PF00171; algedh; 1.
 DR TIGRfam; TIGR00407; proA; 1.
 DR PROSITE; PS01223; PROA; 1.
 DR Oxidoreductase; Proline biosynthesis; NADP.
 KW Oxidoreductase; Proline biosynthesis; NADP.
 SQ SEQUENCE 417 AA; 44985 MW; A280A8A7E9C92268 CRC64;

Query Match 36.8%; Score 7; DB 1; Length 417;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ARAAAR 13
 DB 13 ARAAAR 19

RESULT 12

CESS_HUMAN STANDARD; PRT; 423 AA.
 ID CESS_HUMAN
 AC O9BXW7; Q9BXW8; Q9NWA8; Q9NX41;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cat eye syndrome critical region protein 5 precursor.
 GN CECR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE-21175466; PubMed-11381032;
 RA Footz T.K., Brinkman-Mills P., Banting G.S., Maier S.A., Riazzi M.A.,
 RA Bridgland L.J., Hu S., Birren B., Minochima S., Shimizu N., Pan H.,
 RA Nguyen T., Fang F., Fu Y., Ray L., Wu H., Shaull S., Phan S., Yao Z.,
 RA Chen F., Huan A., Hu P., Wang Q., Loh P., Qi S., Roe B.A.,
 RA McDermid H.E.,
 RT Analysis of the cat eye syndrome critical region in humans and the
 RT region of conserved synteny in mice: a search for candidate genes at
 RT or near the human chromosome 22 pericentromere.;
 RN Genome Res. 11:1053-1070(2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Embryo, and Gastric carcinoma;
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Suqano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Lymph;
 RX PubMed-12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schenfer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan F.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Muzny D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-2;
 CC Name=2;
 CC IsoId=Q9BXW7-1; Sequence=Displayed;
 CC Name=1;
 CC IsoId=Q9BXW7-2; Sequence=VSP_003840;
 CC -!- TISSUE SPECIFICITY: Widely expressed.
 CC -!- MISCELLANEOUS: Candidate gene for the Cat Eye Syndrome (CES), a
 CC developmental disorder associated with the duplication of a 2 Mb
 CC region of 22q11.2. Duplication usually takes in the form of a
 CC supernumerary bisatellited isodicentric chromosome, resulting in
 CC four copies of the region (represents an inv dup(22)(q11)). CES is
 CC characterized clinically by the combination of coloboma of the
 CC iris and anal atresia with fistula, downslanting palpebral
 CC fissures, preauricular tags and/or pits, frequent occurrence of
 CC heart and renal malformations, and normal or near-normal mental
 CC development.
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DR EMBL; AF273271; AAK19152.1; -
 DR EMBL; AF273270; AAK19151.1; -
 DR EMBL; AK001034; BAA91475.1; -
 DR EMBL; AK000461; BAA91180.1; -
 DR EMBL; BC042540; AHA42540.1; -
 DR Genew; HGNC:1843; CECRS.
 DR InterPro; IPR006353; HAD_CECRS.
 DR InterPro; IPR006357; HAD_SF_IIA.
 DR TIGRFAMS; TIGR01456; CECRS.1.
 DR TIGRFAMS; TIGR01460; HAD_SF-ITA; 1.
 KW Signal; Alternative splicing.
 FT SIGNAL 1
 FT CHAIN 23
 FT CHAIN 24 423
 FT POTENTIAL:
 FT CAT EYE SYNDROME CRITICAL REGION PROTEIN
 FT CHAIN 5.
 FT VARSPLIC 1 41
 FT MAAGCVAALGAAGCAGCWAARAAAGAGLGRPARRCVAVGPA
 FT -> MYAFWFLPSFS (in isoform 1).
 FT /FTID-VSP_003840.
 FT CONFLICT 54 54
 FT CONFLICT 86 86
 FT CONFLICT 297 297
 FT CONFLICT V -> F (IN REF. 2; BAA91180).
 FT CONFLICT E -> G (IN REF. 2; BAA91475).
 SQ SEQUENCE 423 AA; 46321 MW; C4D9208A8B888CCE CRC64;
 Query Match 36.8%; Score 7; DB 1; Length 423;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 RAARAAA 12
 Db 19 RAARAAA 25
 RESULT 13
 Y486_MYCLE
 ID Y486_MYCLE STANDARD; PRT; 428 AA.
 AC P54138; Q9CB50;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein ML2443
 DE ML2443 OR U2168F OR B2168_C2_201.
 GN Mycobacterium leprae.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith D.R., Robison K.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TN;
 RX MEDLINE-21128732; PubMed-11234002;
 RA Cole S.T., Eiglmeyer K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RT Massive gene decay in the leprosy bacillus.;
 RL Nature 409:1007-1011(2001).
 CC -!- SIMILARITY: TO M.TUBERCULOSIS RV0486.
 CC
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DR EMBL; U00018; AAA17228.1; ALT_INIT.
DR EMBL; AL583925; CAC31960.1; -.
DR PIR; H87214; H87214.
DR Leproma; ML2443; -.
DR InterPro; IPR001296; Glyco_trans_1.
DR Pfam; PF00534; Glycos_trans_1; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 428 AA; 45291 MW; A14F9F0187E3587C CRC64;

Query Match 36.8%; Score 7; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RRAARAA 11
DB 204 RRAARAA 210
|||||

RESULT 14
VGLX_HSVBS STANDARD; PRT; 444 AA.
AC Q08103;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glycoprotein Gx precursor.
OS Bovine herpesvirus type 1.2 (strain ST).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=45407;
RN [1]

SEQUENCE FROM N.A.
RX MEDLINE=94167875; PubMed=8122370;
RA Leung-Tack P., Audonnet J.F., Riviere M.;
RT "The complete DNA sequence and the genetic organization of the short
RL unique region (US) of the bovine herpesvirus type 1 (ST strain).";
RL Virology 199;409-421(1994).

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DR EMBL; Z33068; CA80603.1; -.
DR PIR; S35783; S35783.
DR InterPro; IPR003363; Herpes_gg.
DR Pfam; PF02400; Herpes_gg; 1.
KW Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 444 GLYCOPROTEIN GX.
FT TRANSMEM 390 414 POTENTIAL.
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 444 AA; 46708 MW; 0145942AA35B05CB CRC64;

Query Match 36.8%; Score 7; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 AARRARA 17
DB 422 AARRARA 428
|||||

RESULT 15
TRME_XANAC STANDARD; PRT; 448 AA.
AC Q8PEH9;
DT 28-FEB-2003 (Rel. 41, Created)

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DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE tRNA modification GTPase trme.
GN TRME OR THDF OR XAC4370.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]

SEQUENCE FROM N.A.
RP STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chamberg F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferio M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spicola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417;459-463(2002).

CC -!- FUNCTION: Exhibits a very high intrinsic GTPase hydrolysis rate.
CC Involved in the biosynthesis of the hypermodified nucleoside 5-
CC methylaminomethyl-2-thiouridine, which is found in the wobble
CC position of some tRNAs (By similarity).
CC -!- SIMILARITY: Belongs to the era/trme family of GTP-binding
CC proteins. Trme subfamily.

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DR EMBL; AE012091; AM39200.1; -.
DR HAMAP; MF_00379; -.
DR InterPro; IPR005289; GTP-binding_dom.
DR InterPro; IPR006073; GTP_OBG.
DR InterPro; IPR005225; Small_GTP.
DR InterPro; IPR004520; ThdF.
DR PRINTS; PR00326; GTP_OBG.
DR TIGRFAMs; TIGR00650; MG442; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR TIGRFAMs; TIGR00450; thdF; 1.
KW tRNA processing; GTP-binding; Complete proteome.
FT NP_BIND 225 232 GTP (POTENTIAL).
FT NP_BIND 272 276 GTP (POTENTIAL).
FT NP_BIND 332 335 GTP (POTENTIAL).
SQ SEQUENCE 448 AA; 47543 MW; B6B43D163D92E3F4 CRC64;

Query Match 36.8%; Score 7; DB 1; Length 448;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAARRA 7
DB 143 ARAARRA 149
|||||

Search completed: August 9, 2003, 16:29:50
Job time : 11.7714 secs

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